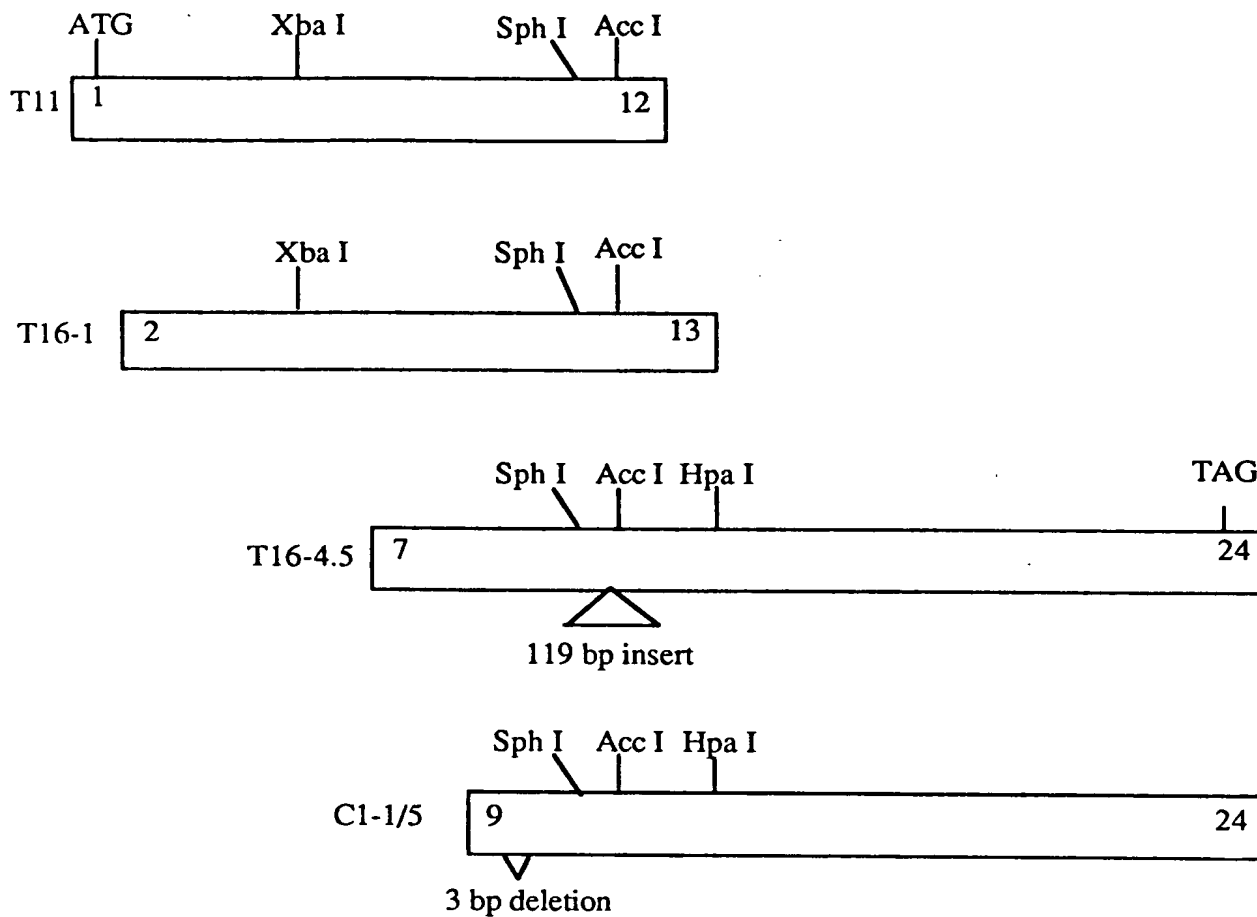# FIGURE 1

PARTIAL cDNA CLONES OF THE CFTR GENE

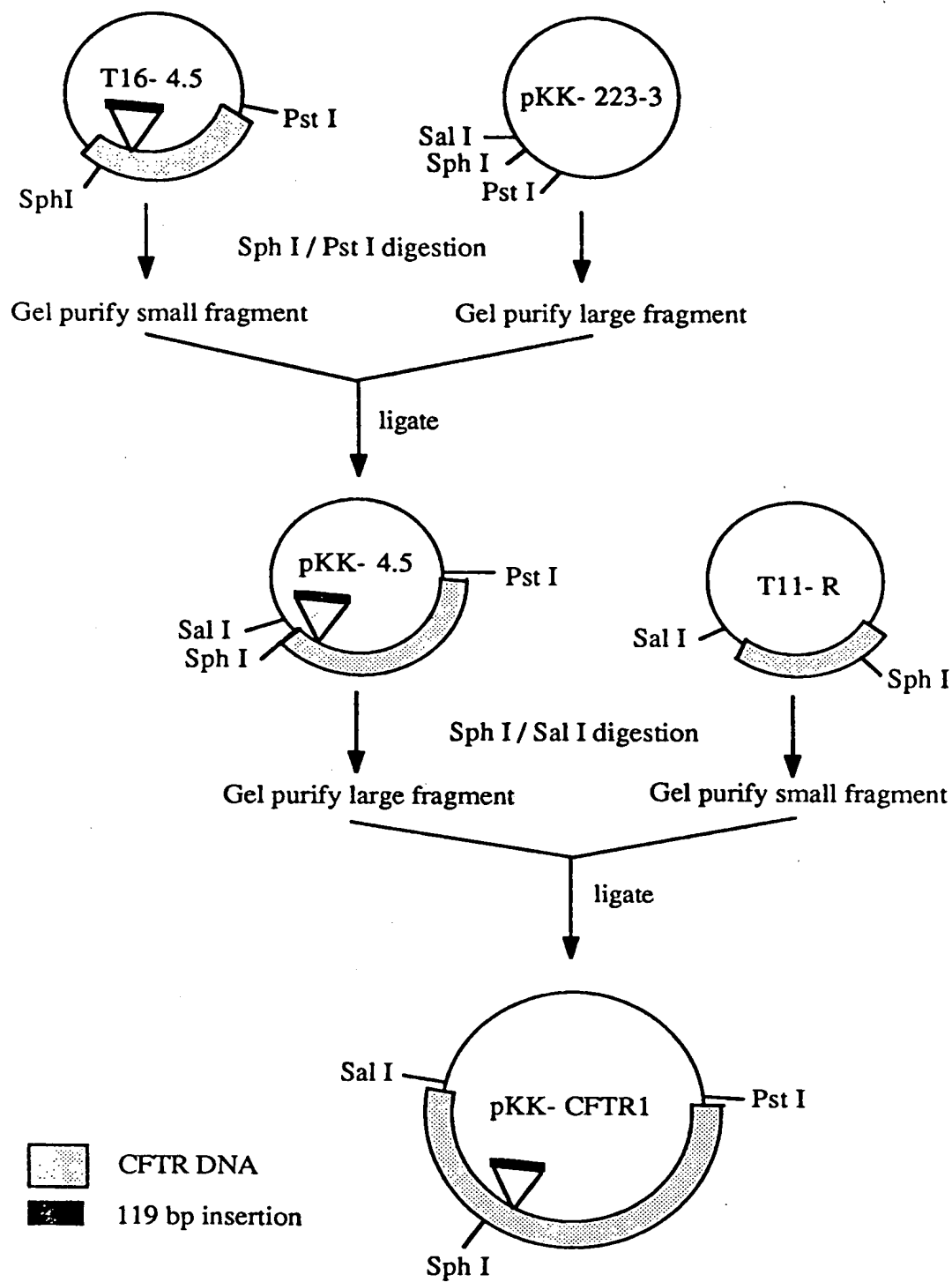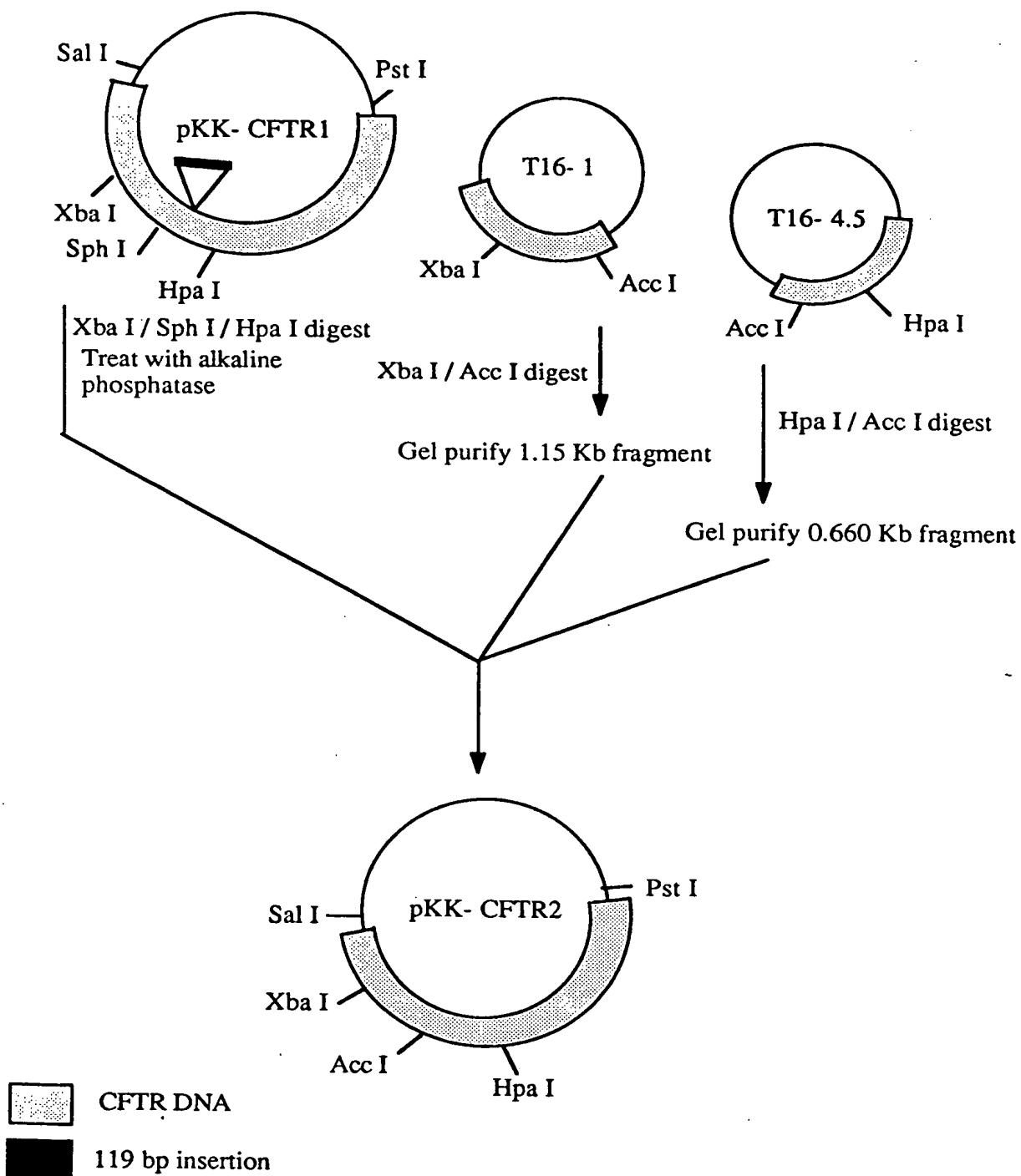# FIGURE 2

STRATEGY FOR CONSTRUCTING pKK- CFTR1

IG 4-9.2

FIGURE 3

CONSTRUCTION OF THE pKK- CFTR2 PLASMID

Sal I

pKK- CFTR1

Pst I

Xba I
Sph I

Hpa I

Xba I / Sph I / Hpa I digest
Treat with alkaline
phosphatase

T16- 1

Xba I   Acc I

Xba I / Acc I digest

Gel purify 1.15 Kb fragment

T16- 4.5

Acc I   Hpa I

Hpa I / Acc I digest

Gel purify 0.660 Kb fragment

Sal I — pKK- CFTR2   — Pst I

Xba I

Acc I   Hpa I

CFTR DNA

119 bp insertion
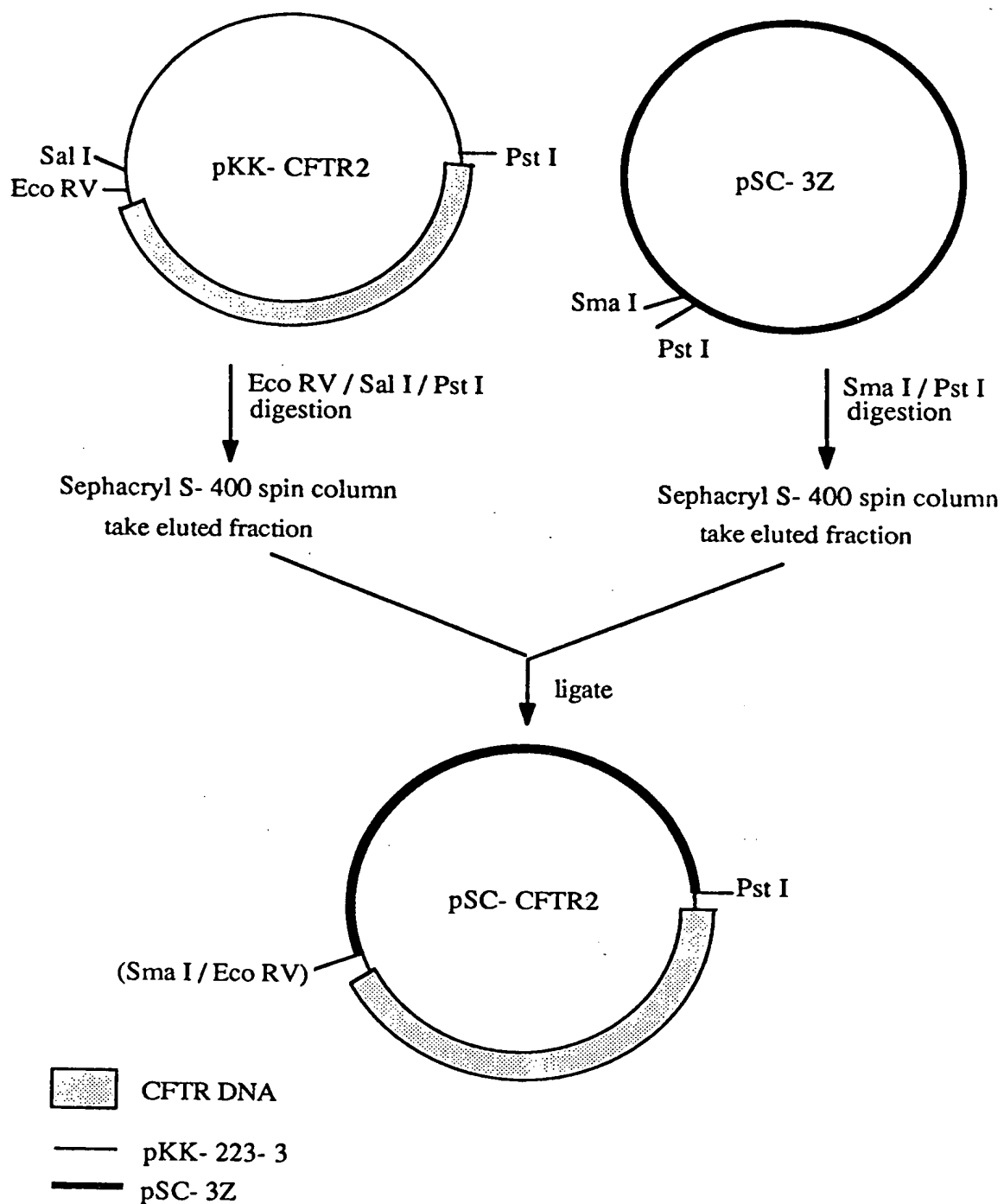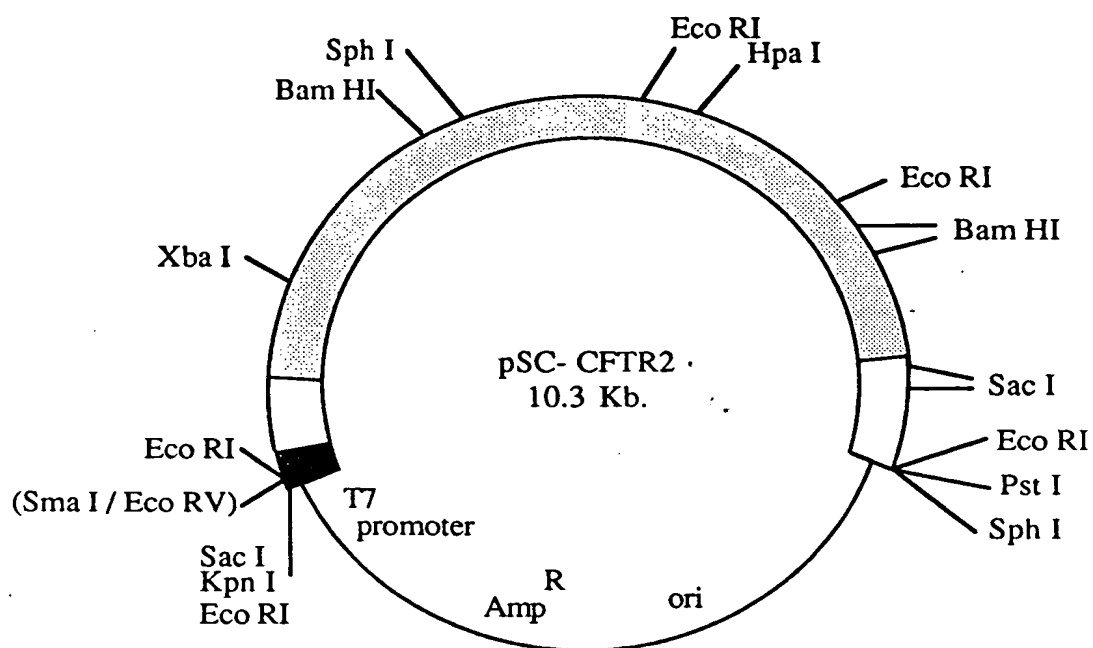
IG 4-9.2

oVer

FIGURE 4
STRATEGY FOR CONSTRUCTING THE pSC- CFTR2 PLASMID

IG 4-9.2

FIGURE 5
MAP OF pSC- CFTR2

Legend:

- CFTR coding region
- CFTR noncoding region
- T11- derived non- CFTR DNA
- ——— pSC- 3Z

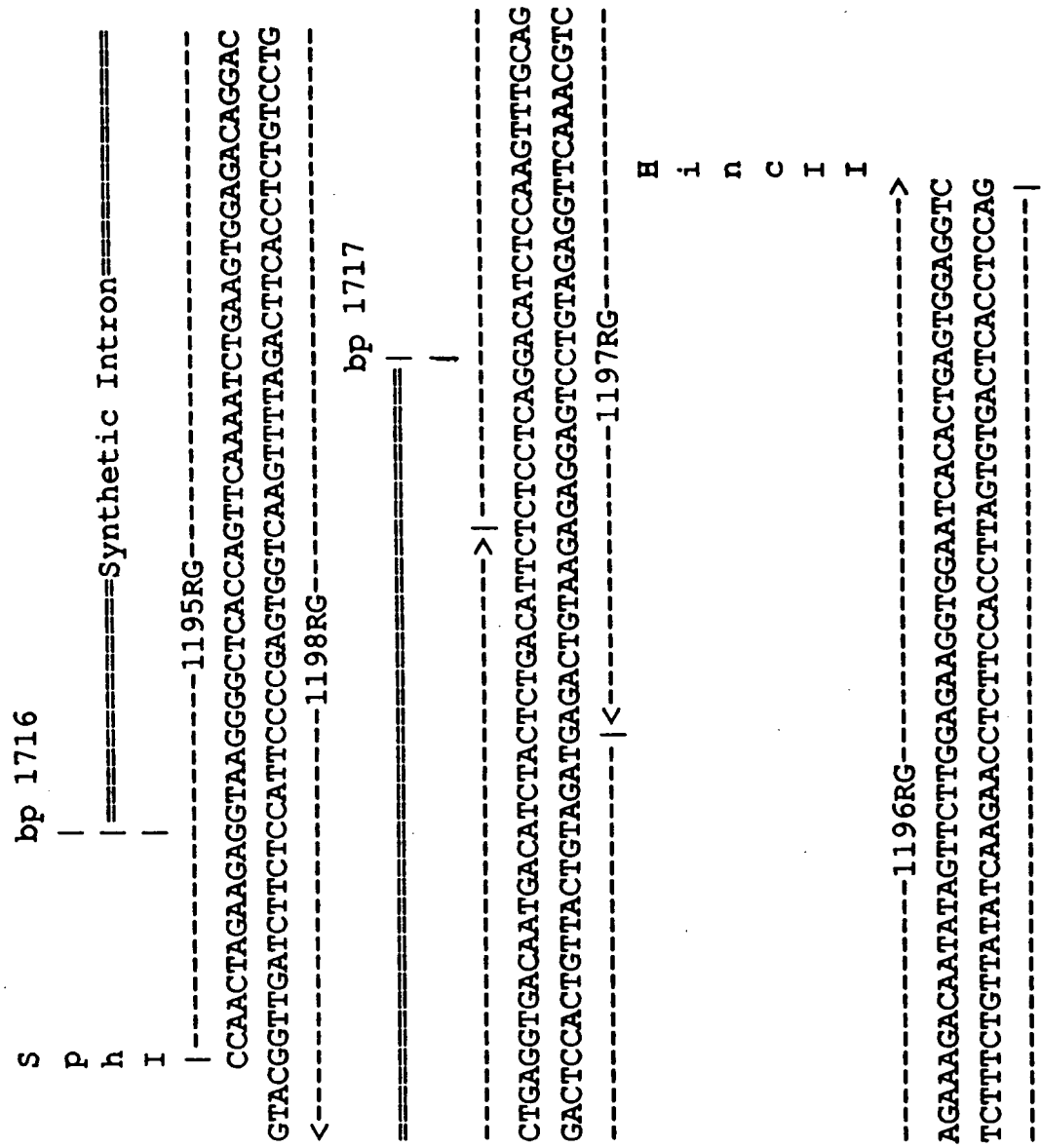IG 4-9.2

FIGURE 6

```
                                  =======Synthetic Intron=======
     bp 1716
s         |--------------------------1195RG--------------------------
p     |        CCAACTAGAGAGGTAAGGGCTCACCAGTTCAAAATCTGAAGTGGAGACAGGAC
h     |        GTACGGTTGATCTTCTCCATTCCCGAGTGGTCAAGTTTTAGACTTCACCTCTGTCCTG
I     |    <----------------------1198RG----------------------

                                  bp 1717
                          ==|
                            |--|
                     >|---------------------------------------
                       CTGAGGTGACAATGACATCTACTCTGACATTCTCTCCTCAGGACATCTCCAAGTTTGCAG
                       GACTCCACTGTTACTGTGATGAGACTGTAAGAGAGGAGTCCTGTAGAGGTTCAAACGTC
             |<----------------1197RG----------------

                                                    H
                                                    i
                                                    n
                                                    c
                                                    I
                                                    I

     -------------1196RG------------------------------------------->
           AGAAAGACAAATATAGTTCTTGGAGAAGGTGGAATCACACTGAGTGGAGTC
           TCTTTCTGTTATATCAAGAACCTCTTCCACCTTAGTGTGACTCACCTCCAG
```

IG 4-9.2

FIGURE 7A

CONSTRUCTION OF THE pKK- CFTR3 cDNA
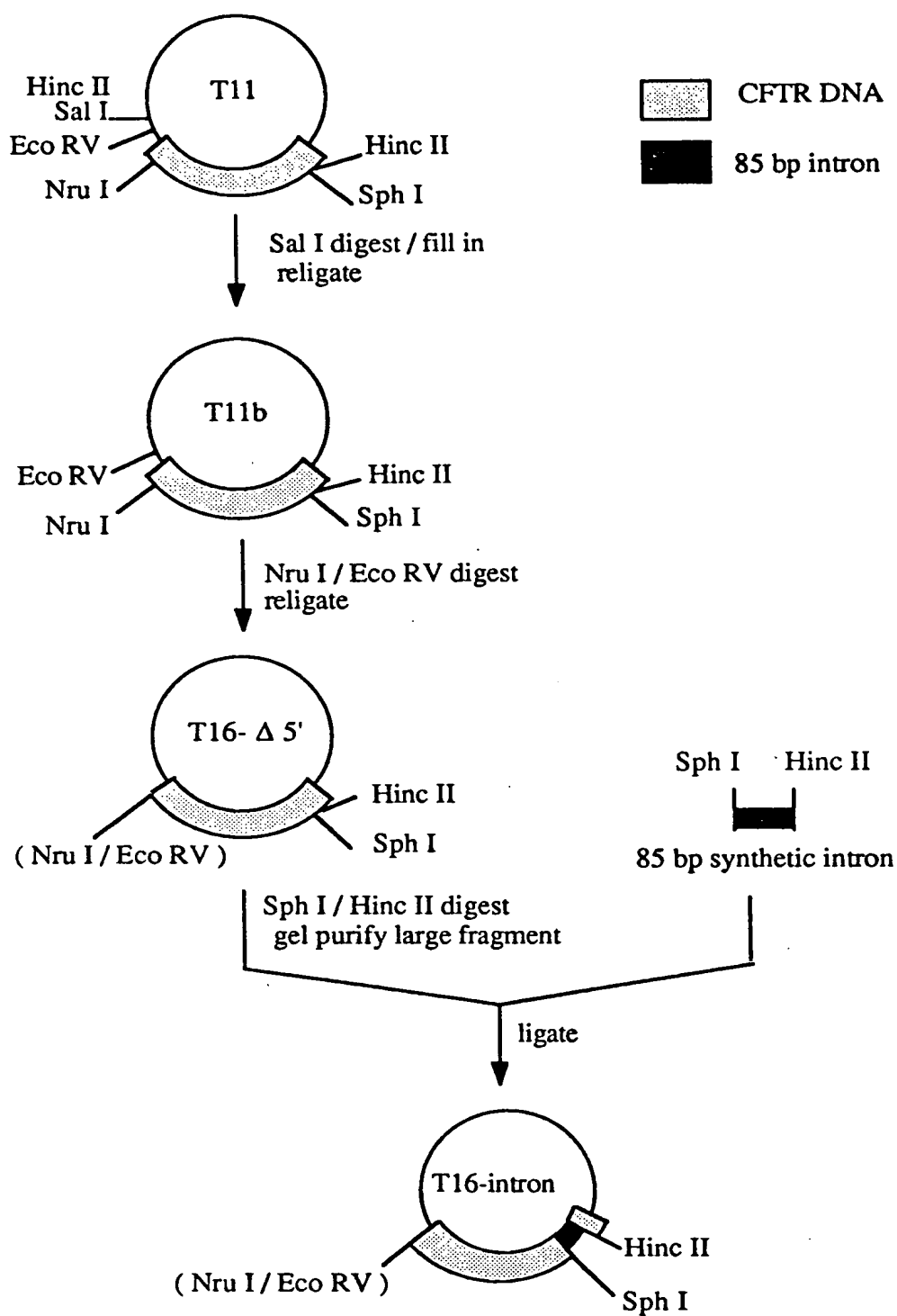

IG 4-9.2

FIGURE 7B

CONSTRUCTION OF THE pKK- CFTR3 CLONE (cont'd.)
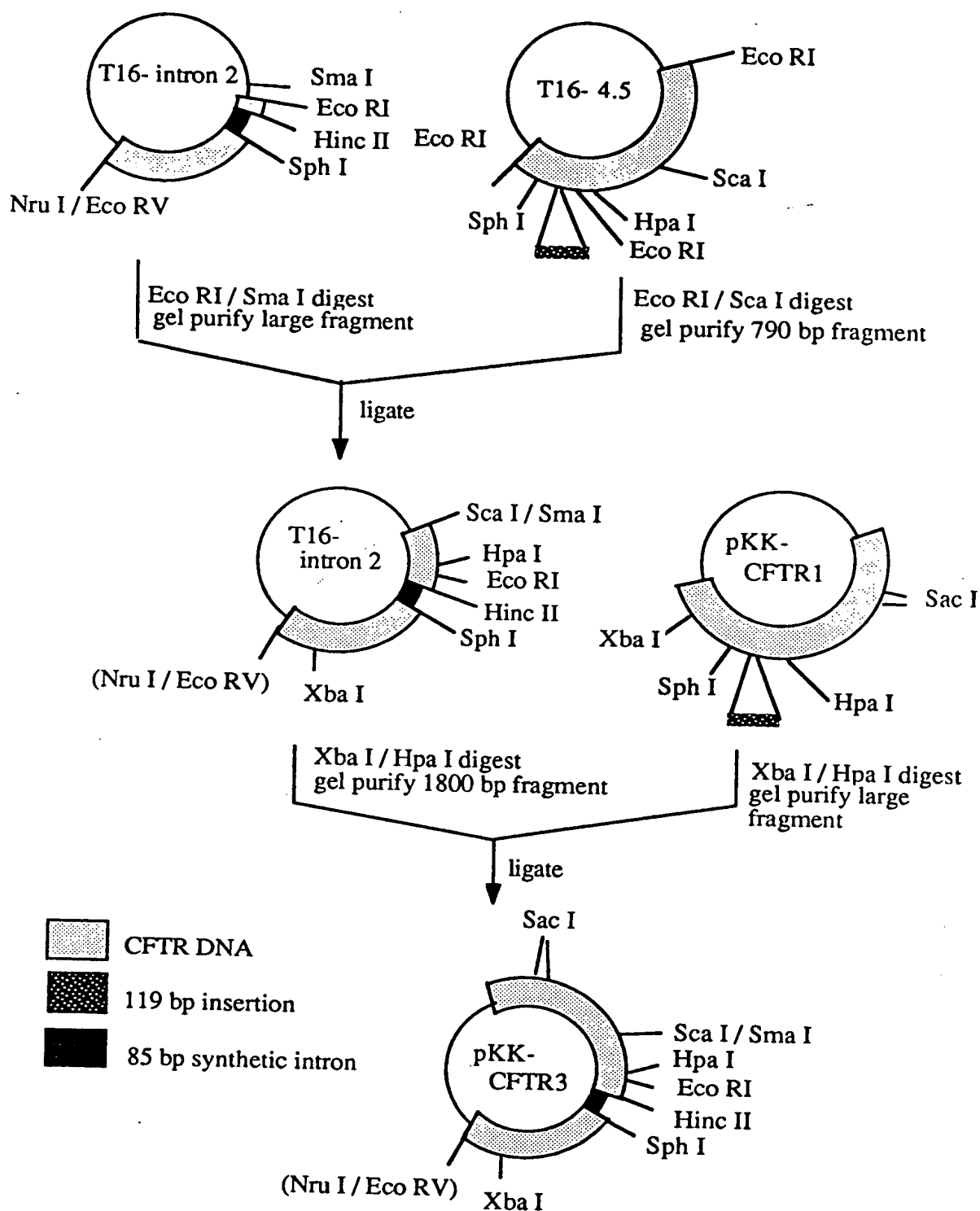
IG 4-9.2

FIGURE 8
MAP OF pKK- CFTR3

Legend:
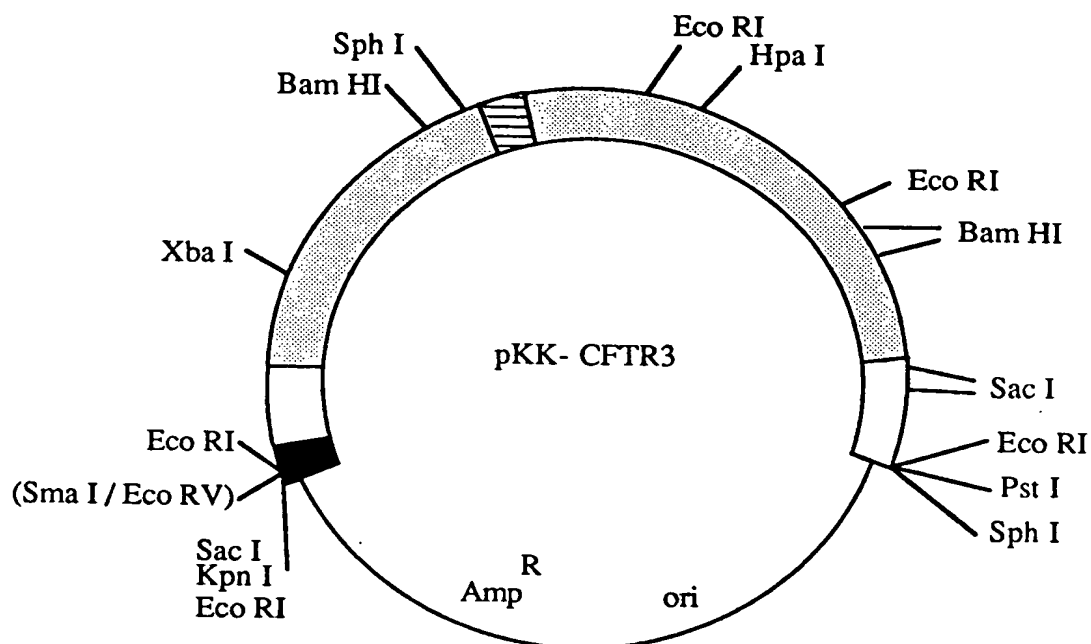
☐ CFTR coding region

☐ CFTR noncoding region

▤ 85 bp intron

■ T11- derived non- CFTR DNA

— pKK- 223- 3

IG 4-9.2

FIGURE 9

Glycosidase:	N-Glycanase	N-Glycanase	Endo. F	Endo. H
CFTR:	C	B	C	C
	− +	− +	− +	− +

200 −

— C
= B
\ A

97.4 −

69 −

| 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 |
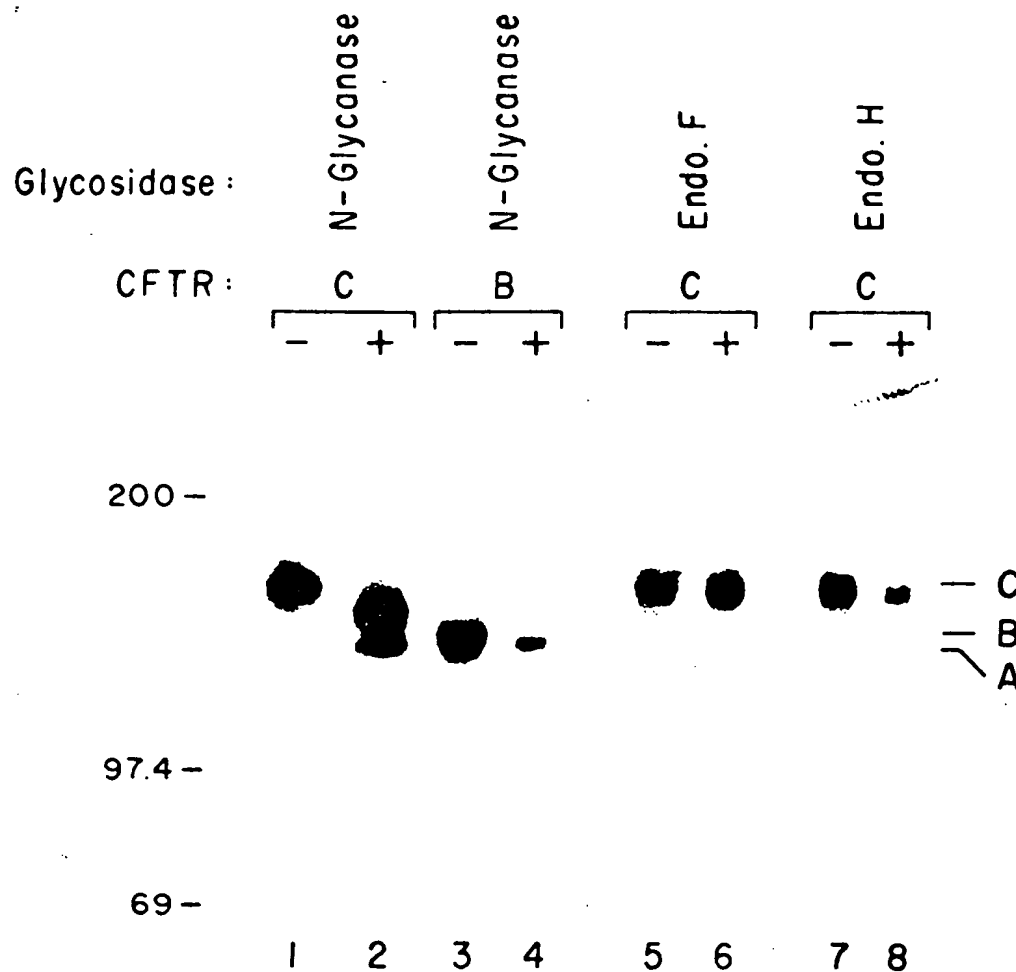
IG 4-9.2

FIGURE 10

FIGURE 11

FIGURE 12

A

B

C

D
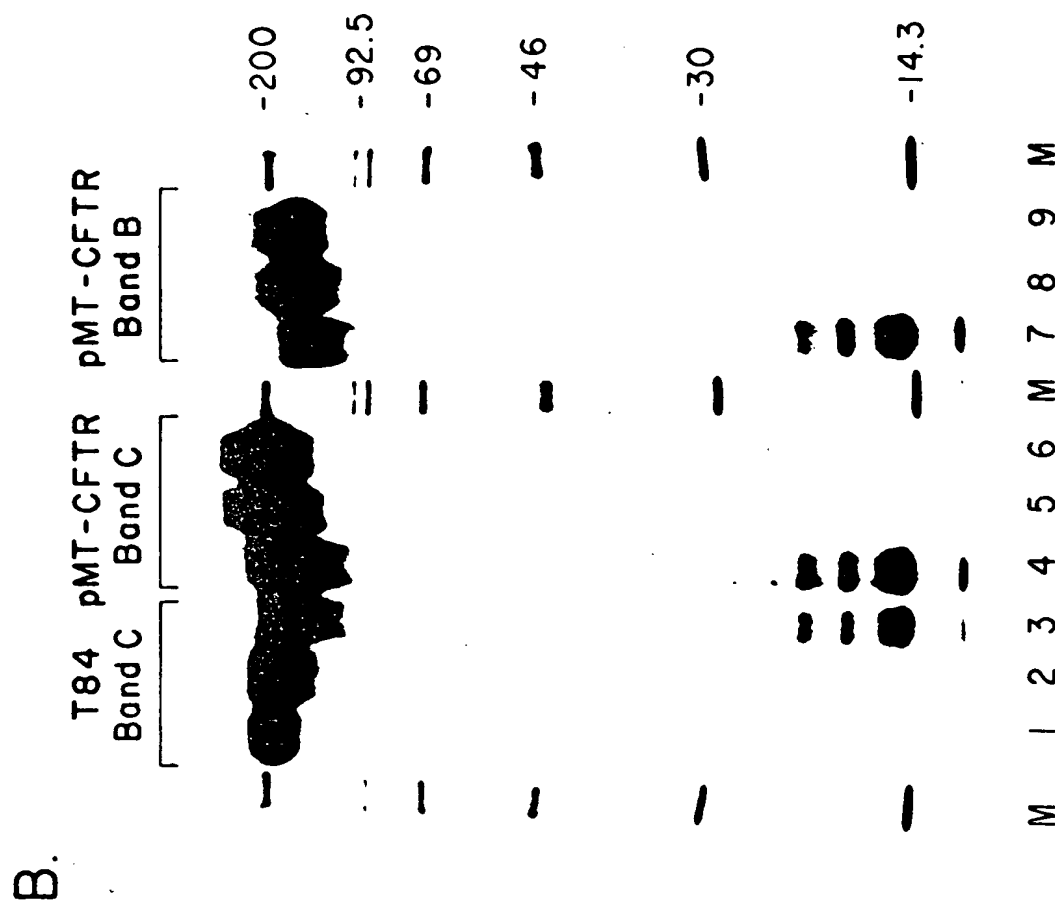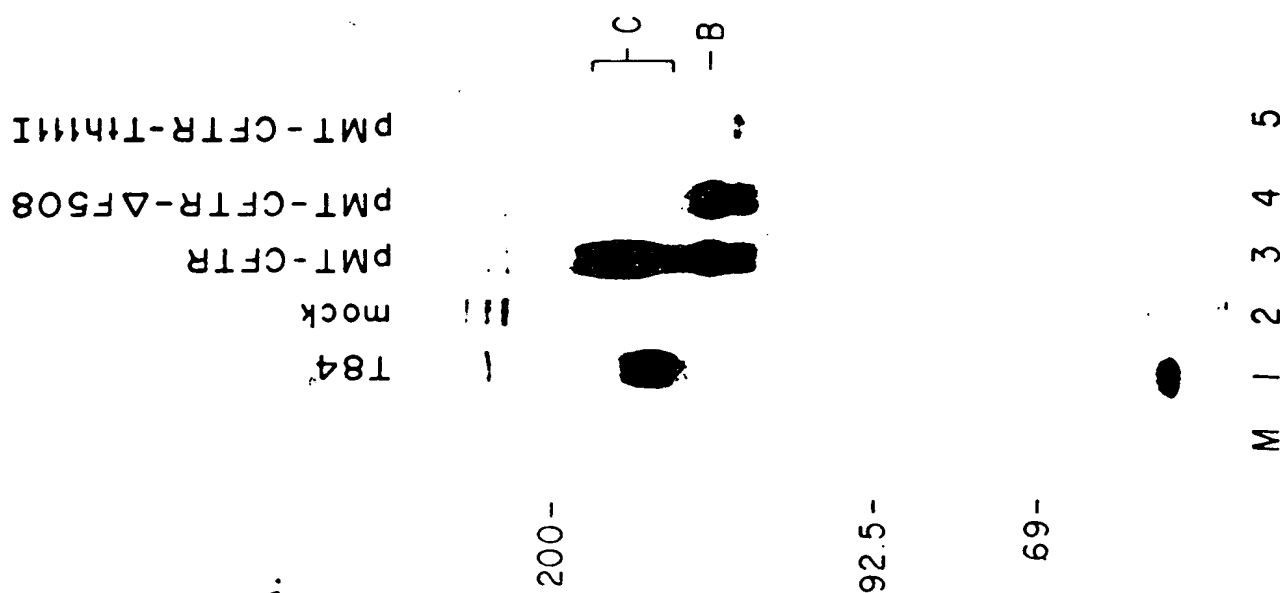
IG 4-9.2

FIGURE 13

IG 4-9.2

TABLE 1 *Figure 15*

```
  1  AATTGGAAGCAAATGACATCACAGCAGGTCAGAGAAAAAGGG      42
 43  TTGAGCGGCAGGCACCCAGAGTAGTAGGTCTTTGGCATTAGG      84
 85  AGCTTGAGCCCAGACGGCCCTAGCAGGGACCCCAGCGCCCGA     126

  1             MetGlnArgSerProLeuGluLysAlaSerValVal      12
127  GAGACCATGCAGAGGTCGCCTCTGGAAAAGGCCAGCGTTGTC     168

 13  SerLysLeuPhePheSerTrpThrArgProIleLeuArgLys      26
169  TCCAAACTTTTTTTCAGCTGGACCAGACCAATTTTGAGGAAA     210

 27  GlyTyrArgGlnArgLeuGluLeuSerAspIleTyrGlnIle      40
211  GGATACAGACAGCGCCTGGAATTGTCAGACATATACCAAATC     252

 41  ProSerValAspSerAlaAspAsnLeuSerGluLysLeuGlu      54
253  CCTTCTGTTGATTCTGCTGACAATCTATCTGAAAAATTGGAA     294

 55  ArgGluTrpAspArgGluLeuAlaSerLysLysAsnProLys      68
295  AGAGAATGGGATAGAGAGCTGGCTTCAAAGAAAAATCCTAAA     336

 69  LeuIleAsnAlaLeuArgArgCysPhePheTrpArgPheMet      82
337  CTCATTAATGCCCTTCGGCGATGTTTTTTCTGGAGATTTATG     378

 83  PheTyrGlyIlePheLeuTyrLeuGlyGluValThrLysAla      96
379  TTCTATGGAATCTTTTTATATTTAGGGGAAGTCACCAAAGCA     420

 97  ValGlnProLeuLeuLeuGlyArgIleIleAlaSerTyrAsp     110
421  GTACAGCCTCTCTTACTGGGAAGAATCATAGCTTCCTATGAC     462

111  ProAspAsnLysGluGluArgSerIleAlaIleTyrLeuGly     124
463  CCGGATAACAAGGAGGAACGCTCTATCGCGATTTATCTAGGC     504

125  IleGlyLeuCysLeuLeuPheIleValArgThrLeuLeuLeu     138
505  ATAGGCTTATGCCTTCTCTTTATTGTGAGGACACTGCTCCTA     546

139  HisProAlaIlePheGlyLeuHisHisIleGlyMetGlnMet     152
547  CACCCAGCCATTTTTGGCCTTCATCACATTGGAATGCAGATG     588

153  ArgIleAlaMetPheSerLeuIleTyrLysLysThrLeuLys     166
589  AGAATAGCTATGTTTAGTTTGATTTATAAGAAGACTTTAAAG     630

167  LeuSerSerArgValLeuAspLysIleSerIleGlyGlnLeu     180
631  CTGTCAAGCCGTGTTCTAGATAAAATAAGTATTGGACAACTT     672

181  ValSerLeuLeuSerAsnAsnLeuAsnLysPheAspGluGly     194
673  GTTAGTCTCCTTTCCAACAACCTGAACAAATTTGATGAAGGA     714
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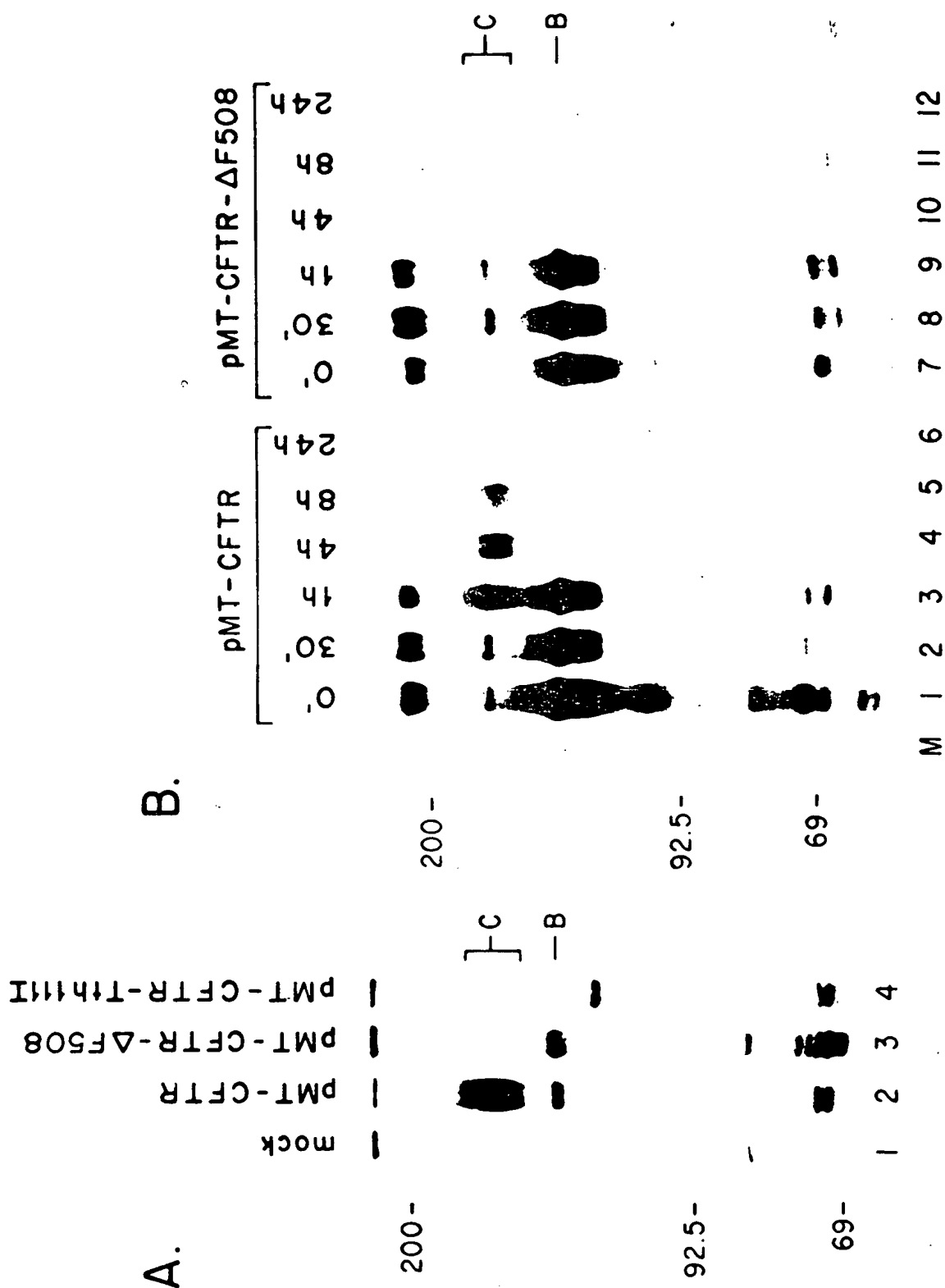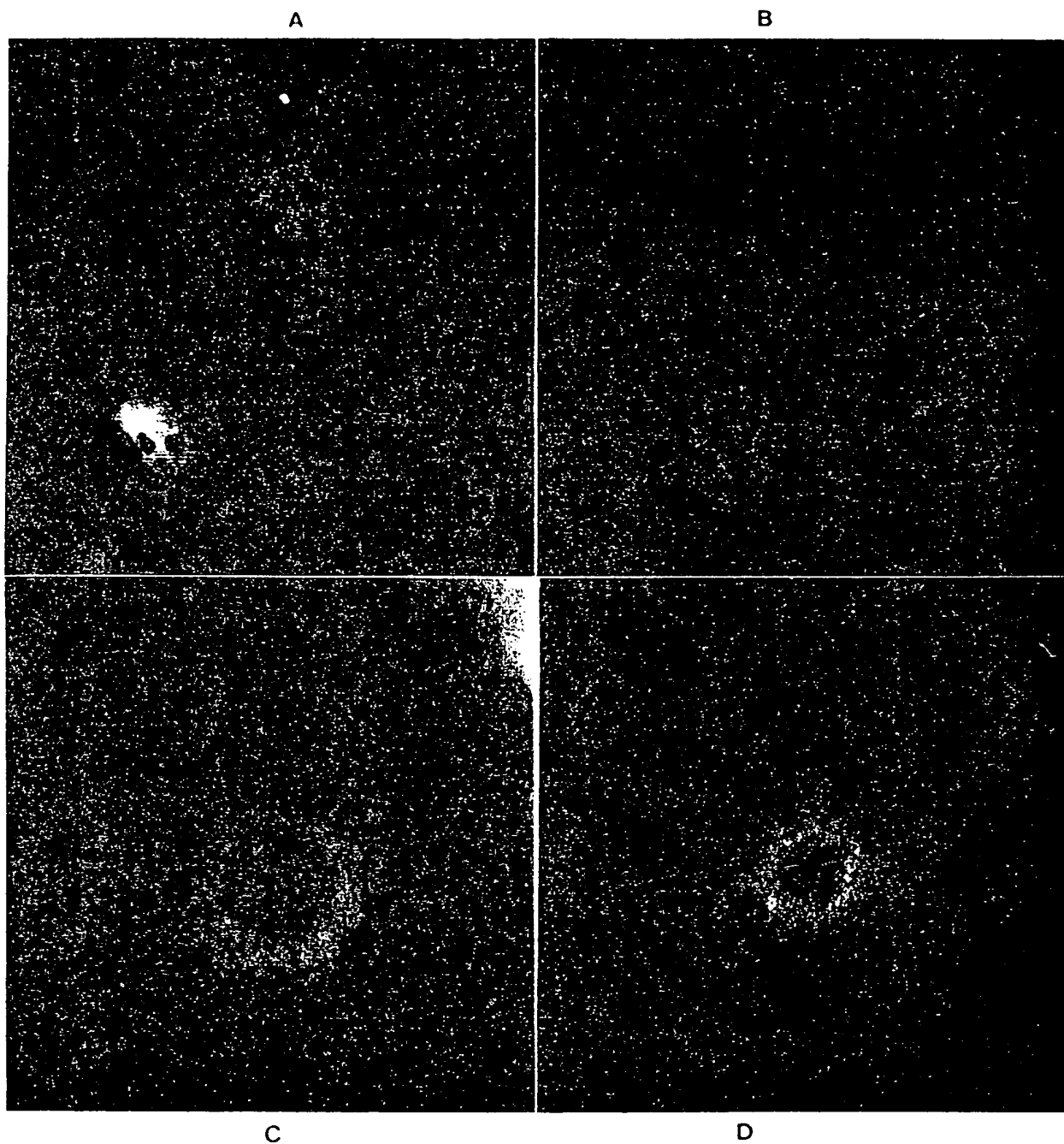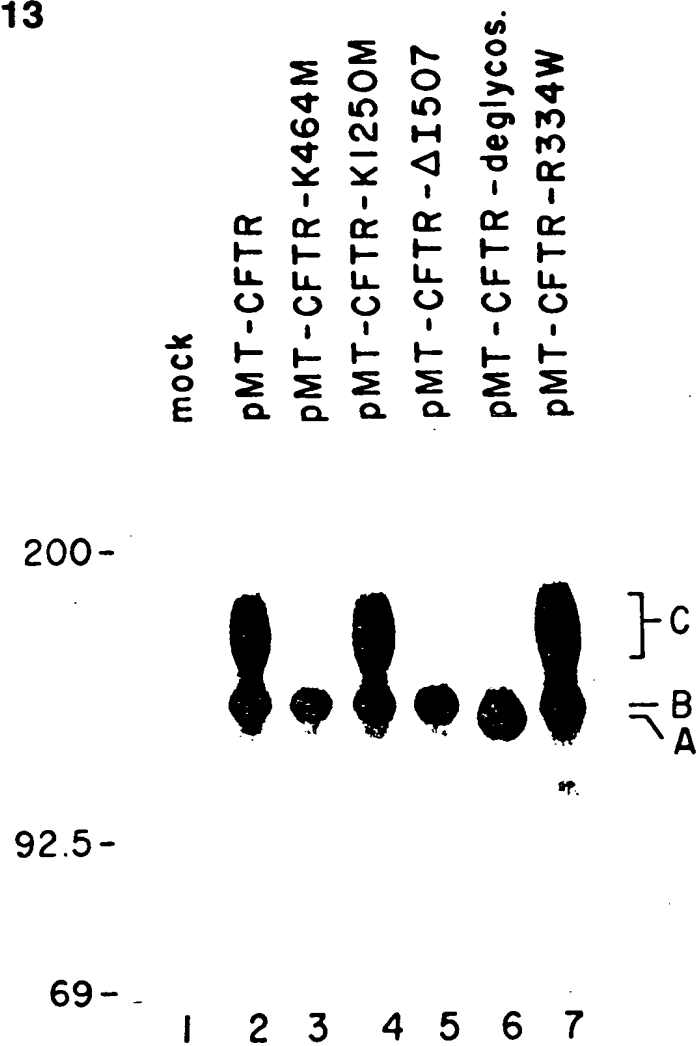
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195   LeuAlaLeuAlaHisPheValTrpIleAlaProLeuGlnVal   208
715   CTTGCATTGGCACATTTCGTGTGGATCGCTCCTTTGCAAGTG   756

209   AlaLeuLeuMetGlyLeuIleTrpGluLeuLeuGlnAlaSer   222
757   GCACTCCTCATGGGGCTAATCTGGGAGTTGTTACAGGCGTCT   798

223   AlaPheCysGlyLeuGlyPheLeuIleValLeuAlaLeuPhe   236
799   GCCTTCTGTGGACTTGGTTTCCTGATAGTCCTTGCCCTTTTT   840

237   GlnAlaGlyLeuGlyArgMetMetMetLysTyrArgAspGln   250
841   CAGGCTGGGCTAGGGAGAATGATGATGAAGTACAGAGATCAG   882

251   ArgAlaGlyLysIleSerGluArgLeuValIleThrSerGlu   264
883   AGAGCTGGGAAGATCAGTGAAAGACTTGTGATTACCTCAGAA   924

265   MetIleGluAsnIleGlnSerValLysAlaTyrCysTrpGlu   278
925   ATGATTGAAAATATCCAATCTGTTAAGGCATACTGCTGGGAA   966

279   GluAlaMetGluLysMetIleGluAsnLeuArgGlnThrGlu   292
967   GAAGCAATGGAAAAAATGATTGAAAACTTAAGACAAACAGAA   1008

293   LeuLysLeuThrArgLysAlaAlaTyrValArgTyrPheAsn   306
1009  CTGAAACTGACTCGGAAGGCAGCCTATGTGAGATACTTCAAT   1050

307   SerSerAlaPhePhePheSerGlyPhePheValValPheLeu   320
1051  AGCTCAGCCTTCTTCTTCTCAGGGTTCTTTGTGGTGTTTTTA   1092

321   SerValLeuProTyrAlaLeuIleLysGlyIleIleLeuArg   334
1093  TCTGTGCTTCCCTATGCACTAATCAAAGGAATCATCCTCCGG   1134

335   LysIlePheThrThrIleSerPheCysIleValLeuArgMet   348
1135  AAAATATTCACCACCATCTCATTCTGCATTGTTCTGCGCATG   1176

349   AlaValThrArgGlnPheProTrpAlaValGlnThrTrpTyr   362
1177  GCGGTCACTCGGCAATTTCCCTGGGCTGTACAAACATGGTAT   1218

363   AspSerLeuGlyAlaIleAsnLysIleGlnAspPheLeuGln   376
1219  GACTCTCTTGGAGCAATAAACAAAATACAGGATTTCTTACAA   1260

377   LysGlnGluTyrLysThrLeuGluTyrAsnLeuThrThrThr   390
1261  AAGCAAGAATATAAGACATTGGAATATAACTTAACGACTACA   1302

391   GluValValMetGluAsnValThrAlaPheTrpGluGluGly   404
1303  GAAGTAGTGATGGAGAATGTAACAGCCTTCTGGGAGGAGGGA   1344

405   PheGlyGluLeuPheGluLysAlaLysGlnAsnAsnAsnAsn   418
1345  TTTGGGGAATTATTTGAGAAAGCAAAACAAAACAATAACAAT   1386
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419    ArgLysThrSerAsnGlyAspAspSerLeuPhePheSerAsn    432
1387   AGAAAAACTTCTAATGGTGATGACAGCCTCTTCTTCAGTAAT    1428

433    PheSerLeuLeuGlyThrProValLeuLysAspIleAsnPhe    446
1429   TTCTCACTTCTTGGTACTCCTGTCCTGAAAGATATTAATTTC    1470

447    LysIleGluArgGlyGlnLeuLeuAlaValAlaGlySerThr    460
1471   AAGATAGAAAGAGGACAGTTGTTGGCGGTTGCTGGATCCACT    1512

461    GlyAlaGlyLysThrSerLeuLeuMetMetIleMetGlyGlu    474
1513   GGAGCAGGCAAGACTTCACTTCTAATGATGATTATGGGAGAA    1554

475    LeuGluProSerGluGlyLysIleLysHisSerGlyArgIle    488
1555   CTGGAGCCTTCAGAGGGTAAAATTAAGCACAGTGGAAGAATT    1596

489    SerPheCysSerGlnPheSerTrpIleMetProGlyThrIle    502
1597   TCATTCTGTTCTCAGTTTTCCTGGATTATGCCTGGCACCATT    1638

503    LysGluAsnIleIlePheGlyValSerTyrAspGluTyrArg    516
1639   AAAGAAAATATCATCTTTGGTGTTTCCTATGATGAATATAGA    1680

517    TyrArgSerValIleLysAlaCysGlnLeuGluGluAspIle    530
1681   TACAGAAGCGTCATCAAAGCATGCCAACTAGAAGAGGACATC    1722

531    SerLysPheAlaGluLysAspAsnIleValLeuGlyGluGly    544
1723   TCCAAGTTTGCAGAGAAAGACAATATAGTTCTTGGAGAAGGT    1764

545    GlyIleThrLeuSerGlyGlyGlnArgAlaArgIleSerLeu    558
1765   GGAATCACACTGAGTGGAGGTCAACGAGCAAGAATTTCTTTA    1806

559    AlaArgAlaValTyrLysAspAlaAspLeuTyrLeuLeuAsp    572
1807   GCAAGAGCAGTATACAAAGATGCTGATTTGTATTTATTAGAC    1848

573    SerProPheGlyTyrLeuAspValLeuThrGluLysGluIle    586
1849   TCTCCTTTTGGATACCTAGATGTTTTAACAGAAAAGAAATA    1890

587    PheGluSerCysValCysLysLeuMetAlaAsnLysThrArg    600
1891   TTTGAAAGCTGTGTCTGTAAACTGATGGCTAACAAAACTAGG    1932

601    IleLeuValThrSerLysMetGluHisLeuLysLysAlaAsp    614
1933   ATTTTGGTCACTTCTAAAATGGAACATTTAAAGAAAGCTGAC    1974

615    LysIleLeuIleLeuHisGluGlySerSerTyrPheTyrGly    628
1975   AAAATATTAATTTTGCATGAAGGTAGCAGCTATTTTTATGGG    2016

629    ThrPheSerGluLeuGlnAsnLeuGlnProAspPheSerSer    642
2017   ACATTTTCAGAACTCCAAAATCTACAGCCAGACTTTAGCTCA    2058
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```
643   LysLeuMetGlyCysAspSerPheAspGlnPheSerAlaGlu   656
2059  AAACTCATGGGATGTGATTCTTTCGACCAATTTAGTGCAGAA   2100

657   ArgArgAsnSerIleLeuThrGluThrLeuHisArgPheSer   670
2101  AGAAGAAATTCAATCCTAACTGAGACCTTACACCGTTTCTCA   2142

671   LeuGluGlyAspAlaProValSerTrpThrGluThrLysLys   684
2143  TTAGAAGGAGATGCTCCTGTCTCCTGGACAGAAACAAAAAAA   2184

685   GlnSerPheLysGlnThrGlyGluPheGlyGluLysArgLys   698
2185  CAATCTTTTAAACAGACTGGAGAGTTTGGGGAAAAAAGGAAG   2226

699   AsnSerIleLeuAsnProIleAsnSerIleArgLysPheSer   712
2227  AATTCTATTCTCAATCCAATCAACTCTATACGAAAATTTTCC   2268

713   IleValGlnLysThrProLeuGlnMetAsnGlyIleGluGlu   726
2269  ATTGTGCAAAAGACTCCCTTACAAATGAATGGCATCGAAGAG   2310

727   AspSerAspGluProLeuGluArgArgLeuSerLeuValPro   740
2311  GATTCTGATGAGCCTTTAGAGAGAAGGCTGTCCTTAGTACCA   2352

741   AspSerGluGlnGlyGluAlaIleLeuProArgIleSerVal   754
2353  GATTCTGAGCAGGGAGAGGCGATACTGCCTCGCATCAGCGTG   2394

755   IleSerThrGlyProThrLeuGlnAlaArgArgArgGlnSer   768
2395  ATCAGCACTGGCCCCACGCTTCAGGCACGAAGGAGGCAGTCT   2436

769   ValLeuAsnLeuMetThrHisSerValAsnGlnGlyGlnAsn   782
2437  GTCCTGAACCTGATGACACACTCAGTTAACCAAGGTCAGAAC   2478

783   IleHisArgLysThrThrAlaSerThrArgLysValSerLeu   796
2479  ATTCACCGAAAGACAACAGCATCCACACGAAAAGTGTCACTG   2520

797   AlaProGlnAlaAsnLeuThrGluLeuAspIleTyrSerArg   810
2521  GCCCCTCAGGCAAACTTGACTGAACTGGATATATATTCAAGA   2562

811   ArgLeuSerGlnGluThrGlyLeuGluIleSerGluGluIle   824
2563  AGGTTATCTCAAGAAACTGGCTTGGAAATAAGTGAAGAAATT   2604

825   AsnGluGluAspLeuLysGluCysLeuPheAspAspMetGlu   838
2605  AACGAAGAAGACTTAAAGGAGTGCCTTTTTGATGATATGGAG   2646

839   SerIleProAlaValThrThrTrpAsnThrTyrLeuArgTyr   852
2647  AGCATACCAGCAGTGACTACATGGAACACATACCTTCGATAT   2688

853   IleThrValHisLysSerLeuIlePheValLeuIleTrpCys   866
2689  ATTACTGTCCACAAGAGCTTAATTTTTGTGCTAATTTGGTGC   2730
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```
 867   LeuValIlePheLeuAlaGluValAlaAlaSerLeuValVal      880
2731   TTAGTAATTTTTCTGGCAGAGGTGGCTGCTTCTTTGGTTGTG      2772

 881   LeuTrpLeuLeuGlyAsnThrProLeuGlnAspLysGlyAsn      894
2773   CTGTGGCTCCTTGGAAACACTCCTCTTCAAGACAAAGGGAAT      2814

 895   SerThrHisSerArgAsnAsnSerTyrAlaValIleIleThr      908
2815   AGTACTCATAGTAGAAATAACAGCTATGCAGTGATTATCACC      2856

 909   SerThrSerSerTyrTyrValPheTyrIleTyrValGlyVal      922
2857   AGCACCAGTTCGTATTATGTGTTTTACATTTACGTGGGAGTA      2898

 923   AlaAspThrLeuLeuAlaMetGlyPhePheArgGlyLeuPro      936
2899   GCCGACACTTTGCTTGCTATGGGATTCTTCAGAGGTCTACCA      2940

 937   LeuValHisThrLeuIleThrValSerLysIleLeuHisHis      950
2941   CTGGTGCATACTCTAATCACAGTGTCGAAAATTTTACACCAC      2982

 951   LysMetLeuHisSerValLeuGlnAlaProMetSerThrLeu      964
2983   AAAATGTTACATTCTGTTCTTCAAGCACCTATGTCAACCCTC      3024

 965   AsnThrLeuLysAlaGlyGlyIleLeuAsnArgPheSerLys      978
3025   AACACGTTGAAAGCAGGTGGGATTCTTAATAGATTCTCCAAA      3066

 979   AspIleAlaIleLeuAspAspLeuLeuProLeuThrIlePhe      992
3067   GATATAGCAATTTTGGATGACCTTCTGCCTCTTACCATATTT      3108

 993   AspPheIleGlnLeuLeuLeuIleValIleGlyAlaIleAla      1006
3109   GACTTCATCCAGTTGTTATTAATTGTGATTGGAGCTATAGCA      3150

1007   ValValAlaValLeuGlnProTyrIlePheValAlaThrVal      1020
3151   GTTGTCGCAGTTTTACAACCCTACATCTTTGTTGCAACAGTG      3192

1021   ProValIleValAlaPheIleMetLeuArgAlaTyrPheLeu      1034
3193   CCAGTGATAGTGGCTTTTATTATGTTGAGAGCATATTTCCTC      3234

1035   GlnThrSerGlnGlnLeuLysGlnLeuGluSerGluGlyArg      1048
3235   CAAACCTCACAGCAACTCAAACAACTGGAATCTGAAGGCAGG      3276

1049   SerProIlePheThrHisLeuValThrSerLeuLysGlyLeu      1062
3277   AGTCCAATTTTCACTCATCTTGTTACAAGCTTAAAAGGACTA      3318

1063   TrpThrLeuArgAlaPheGlyArgGlnProTyrPheGluThr      1076
3319   TGGACACTTCGTGCCTTCGGACGGCAGCCTTACTTTGAAACT      3360

1077   LeuPheHisLysAlaLeuAsnLeuHisThrAlaAsnTrpPhe      1090
3361   CTGTTCCACAAAGCTCTGAATTTACATACTGCCAACTGGTTC      3402
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1091   LeuTyrLeuSerThrLeuArgTrpPheGlnMetArgIleGlu   1104
3403   TTGTACCTGTCAACACTGCGCTGGTTCCAAATGAGAATAGAA   3444

1105   MetIlePheValIlePhePheIleAlaValThrPheIleSer   1118
3445   ATGATTTTTGTCATCTTCTTCATTGCTGTTACCTTCATTTCC   3486

1119   IleLeuThrThrGlyGluGlyGluGlyArgValGlyIleIle   1132
3487   ATTTTAACAACAGGAGAAGGAGAAGGAAGAGTTGGTATTATC   3528

1133   LeuThrLeuAlaMetAsnIleMetSerThrLeuGlnTrpAla   1146
3529   CTGACTTTAGCCATGAATATCATGAGTACATTGCAGTGGGCT   3570

1147   ValAsnSerSerIleAspValAspSerLeuMetArgSerVal   1160
3571   GTAAACTCCAGCATAGATGTGGATAGCTTGATGCGATCTGTG   3612

1161   SerArgValPheLysPheIleAspMetProThrGluGlyLys   1174
3613   AGCCGAGTCTTTAAGTTCATTGACATGCCAACAGAAGGTAAA   3654

1175   ProThrLysSerThrLysProTyrLysAsnGlyGlnLeuSer   1188
3655   CCTACCAAGTCAACCAAACCATACAAGAATGGCCAACTCTCG   3696

1189   LysValMetIleIleGluAsnSerHisValLysLysAspAsp   1202
3697   AAAGTTATGATTATTGAGAATTCACACGTGAAGAAAGATGAC   3738

1203   IleTrpProSerGlyGlyGlnMetThrValLysAspLeuThr   1216
3739   ATCTGGCCCTCAGGGGGCCAAATGACTGTCAAAGATCTCACA   3780

1217   AlaLysTyrThrGluGlyGlyAsnAlaIleLeuGluAsnIle   1230
3781   GCAAAATACACAGAAGGTGGAAATGCCATATTAGAGAACATT   3822

1231   SerPheSerIleSerProGlyGlnArgValGlyLeuLeuGly   1244
3823   TCCTTCTCAATAAGTCCTGGCCAGAGGGTGGGCCTCTTGGGA   3864

1245   ArgThrGlySerGlyLysSerThrLeuLeuSerAlaPheLeu   1258
3865   AGAACTGGATCAGGGAAGAGTACTTTGTTATCAGCTTTTTTG   3906

1259   ArgLeuLeuAsnThrGluGlyGluIleGlnIleAspGlyVal   1272
3907   AGACTACTGAACACTGAAGGAGAAATCCAGATCGATGGTGTG   3948

1273   SerTrpAspSerIleThrLeuGlnGlnTrpArgLysAlaPhe   1286
3949   TCTTGGGATTCAATAACTTTGCAACAGTGGAGGAAAGCCTTT   3990

1287   GlyValIleProGlnLysValPheIlePheSerGlyThrPhe   1300
3991   GGAGTGATACCACAGAAAGTATTTATTTTTTCTGGAACATTT   4032

1301   ArgLysAsnLeuAspProTyrGluGlnTrpSerAspGlnGlu   1314
4033   AGAAAAAACTTGGATCCCTATGAACAGTGGAGTGATCAAGAA   4074
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1315  IleTrpLysValAlaAspGluValGlyLeuArgSerValIle              1328
4075  ATATGGAAAGTTGCAGATGAGGTTGGGCTCAGATCTGTGATA              4116

1329  GluGlnPheProGlyLysLeuAspPheValLeuValAspGly              1342
4117  GAACAGTTTCCTGGGAAGCTTGACTTTGTCCTTGTGGATGGG              4158

1343  GlyCysValLeuSerHisGlyHisLysGlnLeuMetCysLeu              1356
4159  GGCTGTGTCCTAAGCCATGGCCACAAGCAGTTGATGTGCTTG              4200

1357  AlaArgSerValLeuSerLysAlaLysIleLeuLeuLeuAsp              1370
4201  GCTAGATCTGTTCTCAGTAAGGCGAAGATCTTGCTGCTTGAT              4242

1371  GluProSerAlaHisLeuAspProValThrTyrGlnIleIle              1384
4243  GAACCCAGTGCTCATTTGGATCCAGTAACATACCAAATAATT              4284

1385  ArgArgThrLeuLysGlnAlaPheAlaAspCysThrValIle              1398
4285  AGAAGAACTCTAAAACAAGCATTTGCTGATTGCACAGTAATT              4326

1399  LeuCysGluHisArgIleGluAlaMetLeuGluCysGlnGln              1412
4327  CTCTGTGAACACAGGATAGAAGCAATGCTGGAATGCCAACAA              4368

1413  PheLeuValIleGluGluAsnLysValArgGlnTyrAspSer              1426
4369  TTTTTGGTCATAGAAGAGAACAAAGTGCGGCAGTACGATTCC              4410

1427  IleGlnLysLeuLeuAsnGluArgSerLeuPheArgGlnAla              1440
4411  ATCCAGAAACTGCTGAACGAGAGGAGCCTCTTCCGGCAAGCC              4452

1441  IleSerProSerAspArgValLysLeuPheProHisArgAsn              1454
4453  ATCAGCCCCTCCGACAGGGTGAAGCTCTTTCCCCACCGGAAC              4494

1455  SerSerLysCysLysSerLysProGlnIleAlaAlaLeuLys              1468
4495  TCAAGCAAGTGCAAGTCTAAGCCCCAGATTGCTGCTCTGAAA              4536

1469  GluGluThrGluGluGluValGlnAspThrArgLeuEnd              1482
4537  GAGGAGACAGAAGAAGAGGTGCAAGATACAAGGCTTTAGAGA              4578
4579  GCAGCATAAATGTTGACATGGGACATTTGCTCATGGAATTGG              4620
4621  AGCTCGTGGGACAGTCACCTCATGGAATTGGAGCTCGTGGAA              4662
4663  CAGTTACCTCTGCCTCAGAAAACAAGGATGAATTAAGTTTTT              4704
4705  TTTTAAAAAAGAAACATTTGGTAAGGGGAATTGAGGACACTG              4746
4747  ATATGGGTCTTGATAAATGGCTTCCTGGCAATAGTCAAATTG              4788
4789  TGTGAAAGGTACTTCAAATCCTTGAAGATTTACCACTTGTGT              4830
4831  TTTGCAAGCCAGATTTTCCTGAAAACCCTTGCCATGTGCTAG              4872
4873  TAATTGGAAAGGCAGCTCTAAA   4894
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